

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (currently amended) A method of creating hybrid proteins having a common biological activity comprising the steps of:

(a) selecting at least five positions that are mismatched in a sequence alignment of at least two parent proteins that have 60% or greater amino acid similarity and at least one common biological activity;

(a) (b) creating a library comprising 32 or more nucleic acids encoding a plurality of hybrid protein members, wherein the members differ from set of at least two parent proteins with corresponding amino acids, wherein the library is created by introducing a degenerate codon at the at least five mismatched positions where a degenerate codon at a mismatched position alternatively encodes at least two parent amino acid residues at each of the five mismatched positions, and wherein the parental codon that occurs at each of the five mismatched positions is independent of the parental codon that occurs at the other of the five mismatched sites; and

i. where the parent proteins are homologous proteins having greater than 60% amino acid similarity to each other and having at least one common biological activity,

ii. where a majority of the library members have a greater than 60% amino acid similarity to any of the parent proteins, and

iii. where the majority of differences between the library members and the parent proteins are confined to those corresponding amino acids that differ among the parent proteins;

(c) (b) expressing protein from at least one library member to create at least one hybrid protein;

(d) (e) selecting at least one protein expressed from the library having a common biological activity of the parent proteins.

2. (original) The method of claim 1, wherein the parent proteins are enzymes.
3. (original) The method of claim 1, wherein the parent proteins are isozymes.
4. (original) The method of claim 1, wherein the parent proteins are polymerases.
5. (currently amended) The method of claim 1, wherein the parent proteins have greater than 80% amino acid similarity to each other and the majority of the library members have greater than 80% amino acid similarity to any of the ~~wild-type~~ parent proteins.
- 6.-16 (cancelled)
17. (new) The method of claim 4, wherein the polymerases are thermostable polymerases.
18. (new) The method of claim 4, wherein at least one polymerase is from *Pyrococcus furiosus*.
19. (new) The method of claim 1, wherein at least twenty mismatched positions are selected and degeneracies are introduced at the twenty mismatched positions.